

SEQUENCE LISTING

dtl
18/15

(1) GENERAL INFORMATION:

- (i) APPLICANT: HU, JING-SHAN
OLSEN, HENRIK
ROSEN, CRAIG G.
- (ii) TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING VASCULAR
ENDOTHELIAL GROWTH FACTOR 3 POLYPEPTIDES AND METHODS FOR
PRODUCING THE POLYPEPTIDES
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVE, NW
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/469,641
 - (B) FILING DATE: 06-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEFFE, ERIC K.
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.1040000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..663
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	AGA	AGG	TGT	AGA	ATA	AGT	GGG	AGG	CCC	CCG	GCG	CCC	CCC	GGT	GTC	48
Met	Arg	Arg	Cys	Arg	Ile	Ser	Gly	Arg	Pro	Pro	Ala	Pro	Pro	Gly	Val	
1				5					10					15		
CCC	GCC	CAG	GCC	CCT	GTC	TCC	CAG	CCT	GAT	GCC	CCT	GGC	CAC	CAG	AGG	96
Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln	Arg	
			20					25					30			
AAA	GTG	GTG	TCA	TGG	ATA	GAT	GTG	TAT	ACT	CGC	GCT	ACC	TGC	CAG	CCC	144
Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln	Pro	
		35					40					45				
CGG	GAG	GTG	GTG	GTG	CCC	TTG	ACT	GTG	GAG	CTC	ATG	GGC	ACC	GTG	GCC	192
Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val	Ala	
	50					55					60					
AAA	CAG	CTG	GTG	CCC	AGC	TGC	GTG	ACT	GTG	CAG	CGC	TGT	GGT	GGC	TGC	240
Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys	
65					70					75					80	
TGC	CCT	GAC	GAT	GGC	CTG	GAG	TGT	GTG	CCC	ACT	GGG	CAG	CAC	CAA	GTC	288
Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val	
				85					90					95		
CGG	ATG	CAG	ATC	CTC	ATG	ATC	CGG	TAC	CCG	AGC	AGT	CAG	CTG	GGG	GAG	336
Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu	
			100					105					110			
ATG	TCC	CTG	GAA	GAA	CAC	AGC	CAG	TGT	GAA	TGC	AGA	CCT	AAA	AAA	AAG	384
Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys	
		115					120					125				
GAC	AGT	GCT	GTG	AAG	CCA	GAC	AGG	GCT	GCT	ACT	CCC	CAC	CAC	CGT	CCC	432
Asp	Ser	Ala	Val	Lys	Pro	Asp	Arg	Ala	Ala	Thr	Pro	His	His	Arg	Pro	
	130					135					140					
CAG	CCC	CGT	TCT	GTT	CCG	GGC	TGG	GAC	TCT	GCC	CCC	GGA	GCA	CCC	TCC	480
Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	Pro	Ser	
145					150					155					160	
CCA	GCT	GAC	ATC	ACC	CAA	TCC	CAC	TCC	AGC	CCC	AGG	CCC	CTC	TGC	CCA	528
Pro	Ala	Asp	Ile	Thr	Gln	Ser	His	Ser	Ser	Pro	Arg	Pro	Leu	Cys	Pro	
				165					170					175		
CGC	TGC	ACC	CAG	CAC	CAC	CAG	TGC	CCT	GAC	CCC	CGG	ACC	TGC	CGC	TGC	576
Arg	Cys	Thr	Gln	His	His	Gln	Cys	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	
			180					185					190			
CGC	TGT	CGA	CGC	CGC	AGC	TTC	CTC	CGT	TGT	CAA	GGG	CGG	GGC	TTA	GAG	624
Arg	Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu	
		195					200				205					
CTC	AAC	CCA	GAC	ACC	TGC	AGG	TGC	CGG	AAG	CTG	CGA	AGG	TGA			666
Leu	Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg				
	210					215					220					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Arg	Cys	Arg	Ile	Ser	Gly	Arg	Pro	Pro	Ala	Pro	Pro	Gly	Val
1				5					10					15	
Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln	Arg
			20					25					30		
Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln	Pro
		35					40					45			
Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val	Ala
	50					55					60				
Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys
65					70					75					80
Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val
				85					90					95	
Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu
			100					105					110		
Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys
		115					120					125			
Asp	Ser	Ala	Val	Lys	Pro	Asp	Arg	Ala	Ala	Thr	Pro	His	His	Arg	Pro
	130						135					140			
Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	Pro	Ser
145					150					155					160
Pro	Ala	Asp	Ile	Thr	Gln	Ser	His	Ser	Ser	Pro	Arg	Pro	Leu	Cys	Pro
				165					170					175	
Arg	Cys	Thr	Gln	His	His	Gln	Cys	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys
			180					185					190		
Arg	Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu
		195					200					205			
Leu	Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg			
210						215					220				

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
GCATGGATCC CAGCCTGATG CCCCTGGCC 29

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
GCATTCTAGA CCCTGCTGAG TCTGAAAAGC 30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
GACTGCATGC ACCAGAGGAA AGTGGTGTC 29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
GACTAGATCT CCTTCGCAGC TTCCGGCAC 29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro	Xaa	Cys	Val	Xaa	Xaa	Xaa	Arg	Cys	Xaa	Gly	Cys	Cys	Asn
1				5					10				

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	Glu	Gly
			20					25					30		
Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln
		35					40					45			
Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu
	50					55					60				
Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu
65					70					75					80
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro
				85					90					95	
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His
			100					105					110		
Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys
		115					120					125			
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Lys	Lys	Ser	Val
	130					135					140				
Arg	Gly	Lys	Gly	Lys	Gly	Gln	Lys	Arg	Lys	Arg	Lys	Lys	Ser	Arg	Tyr
145					150					155					160
Lys	Ser	Trp	Ser	Val	Pro	Cys	Gly	Pro	Cys	Ser	Glu	Arg	Arg	Lys	His
				165					170					175	
Leu	Phe	Val	Gln	Asp	Pro	Gln	Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr
			180					185					190		
Asp	Ser	Arg	Cys	Lys	Ala	Arg	Gln	Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys

195

200

205

Arg Cys Asp Lys Pro Arg Arg
210 215